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7-3-02  
P.Z.

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/840,704

DATE: 12/19/2001  
 TIME: 13:05:37

Input Set : N:\Crf3\RULE60\09840704.raw  
 Output Set: N:\CRF3\12192001\I840704.raw

1 <110> APPLICANT: Dedhar, Shoukat  
 2 Hannigan, Greg  
 3 <120> TITLE OF INVENTION: Integrin-Linked Kinase and its Uses  
 4 <130> FILE REFERENCE: KIN-2CON  
 5 <140> CURRENT APPLICATION NUMBER: 09/840,704  
 6 <141> CURRENT FILING DATE: 2001-04-23  
 7 <150> PRIOR APPLICATION NUMBER: 09/566,906  
 8 <151> PRIOR FILING DATE: 2000-05-09  
 9 <150> PRIOR APPLICATION NUMBER: US08/752,345  
 10 <151> PRIOR FILING DATE: 1996-11-19  
 11 <160> NUMBER OF SEQ ID NOS: 16  
 12 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 14 <210> SEQ ID NO: 1  
 15 <211> LENGTH: 1789  
 16 <212> TYPE: DNA  
 17 <213> ORGANISM: H. sapiens  
 18 <220> FEATURE:  
 19 <221> NAME/KEY: CDS  
 20 <222> LOCATION: (157)...(1512)  
 W--> 21 <221> NAME/KEY: Other  
 22 <222> LOCATION: (0)...(0)  
 23 <400> SEQUENCE: 1

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APR 01 2002

TECH CENTER 1600/2900

ENTERED

RECEIVED

24	gaattcatct	gtcgactgct	accacgggag	ttcccccggag	aaggatctg	tcgcggagt	APP 01/2002	60
25	cccgaggata	aagcttgggg	ttcatcctcc	ttccctggat	cactccacag	tcctcaggct	TECH CENTER 1600/2900	120
26	tccccaatcc	aggggactcg	gcgcgggac	gctgct	atg	tcgcggat		174
27						Met Asp Asp Ile Phe Thr		
28					1	5		
29	cag tgc cgg gag ggc aac gca gtc gcc gtt	cgc ctg tgg	ctg gac aac					222
30	Gln Cys Arg Glu Gly Asn Ala Val	Ala Val Arg Leu Trp Leu Asp Asn						
31	10	15	20					
32	acg gag aac gac ctc aac cag	ggg gac gat cat	ggc ttc tcc ccc ttg					270
33	Thr Glu Asn Asp Leu Asn Gln	Gly Asp Asp His	Gly Phe Ser Pro Leu					
34	25	30	35					
35	cac tgg gcc tgc cga gag ggc	cgc tct gct gtg	gtt gag atg ttg atc					318
36	His Trp Ala Cys Arg Glu Gly Arg Ser Ala Val	Val Val Glu Met Leu Ile						
37	40	45	50					
38	atg cgg ggg gca cgg atc aat	gta atg aac cgt	ggg gat gac acc ccc					366
39	Met Arg Gly Ala Arg Ile Asn Val	Met Asn Arg Gly Asp Asp Thr Pro						
40	55	60	65	70				
41	ctg cat ctg gca gcc agt	cat gga cac cgt	gat att gta cag aag cta					414
42	Leu His Leu Ala Ala Ser His Gly His Arg Asp Ile Val Gln Lys Leu							
43	75	80	85					
44	ttg cag tac aag gca gac atc aat	gca gtg aat gaa cac	ggg aat gtg					462
45	Leu Gln Tyr Lys Ala Asp Ile Asn Ala Val	Asn Glu His Gly Asn Val						
46	90	95	100					
47	ccc ctg cac tat gcc tgt ttt	tgg ggc caa gat	caa gtg gca gag gac					510
48	Pro Leu His Tyr Ala Cys Phe Trp Gly Gln Asp Gln Val Ala Glu Asp							

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49	105	110	115															
50	ctg	gtg	gca	aat	ggg	gcc	ctt	gtc	agc	atc	tgt	aac	aag	tat	gga	gag		558
51	Leu	Val	Ala	Asn	Gly	Ala	Leu	Val	Ser	Ile	Cys	Asn	Lys	Tyr	Gly	Glu		
52	120		125		130													
53	atg	cct	gtg	gac	aaa	gcc	aag	gca	ccc	ctg	aga	gag	ctt	ctc	cga	gag		606
54	Met	Pro	Val	Asp	Lys	Ala	Lys	Ala	Pro	Leu	Arg	Glu	Leu	Leu	Arg	Glu		
55	135		140		145		150											
56	cgg	gca	gag	aag	atg	ggc	cag	aat	ctc	aac	cgt	att	cca	tac	aag	gac		654
57	Arg	Ala	Glu	Lys	Met	Gly	Gln	Asn	Leu	Asn	Arg	Ile	Pro	Tyr	Lys	Asp		
58	155		160		165													
59	aca	tcc	tgg	aag	ggg	acc	acc	cgc	act	cgg	ccc	cga	aat	gga	acc	ctg		702
60	Thr	Phe	Trp	Lys	Gly	Thr	Thr	Arg	Thr	Arg	Pro	Arg	Asn	Gly	Thr	Leu		
61	170		175		180													
62	aac	aaa	cac	tct	ggc	att	gac	ttc	aaa	cag	ctt	aac	ttc	ctg	acg	aag		750
63	Asn	Lys	His	Ser	Gly	Ile	Asp	Phe	Lys	Gln	Leu	Asn	Phe	Leu	Thr	Lys		
64	185		190		195													
65	ctc	aac	gag	aat	cac	tct	gga	gag	cta	tgg	aag	ggc	cgc	tgg	cag	ggc		798
66	Leu	Asn	Glu	Asn	His	Ser	Gly	Glu	Leu	Trp	Lys	Gly	Arg	Trp	Gln	Gly		
67	200		205		210													
68	aat	gac	att	gtc	gtg	aag	gtg	ctg	aag	gtt	cga	gac	tgg	agt	aca	agg		846
69	Asn	Asp	Ile	Val	Val	Lys	Val	Leu	Lys	Val	Arg	Asp	Trp	Ser	Thr	Arg		
70	215		220		225		230											
71	aag	agc	agg	gac	ttc	aat	gaa	gag	tgt	ccc	cgg	ctc	agg	att	ttc	tcg		894
72	Lys	Ser	Arg	Asp	Phe	Asn	Glu	Glu	Cys	Pro	Arg	Leu	Arg	Ile	Phe	Ser		
73	235		240		245													
74	cat	cca	aat	gtg	ctc	cca	gtg	cta	ggt	gcc	tgc	cag	tct	cca	cct	gct		942
75	His	Pro	Asn	Val	Leu	Pro	Val	Leu	Gly	Ala	Cys	Gln	Ser	Pro	Pro	Ala		
76	250		255		260													
77	cct	cac	cct	act	ctc	atc	aca	cac	tgg	atg	ccg	tat	gga	tcc	ctc	tac		990
78	Pro	His	Pro	Thr	Leu	Ile	Thr	His	Trp	Met	Pro	Tyr	Gly	Ser	Leu	Tyr		
79	265		270		275													
80	aat	gta	cta	cat	gaa	ggc	acc	aat	ttc	gtc	gtg	gac	cag	acg	cag	gct		1038
81	Asn	Val	Leu	His	Glu	Gly	Thr	Asn	Phe	Val	Val	Asp	Gln	Ser	Gln	Ala		
82	280		285		290													
83	gtg	aag	ttt	gct	ttg	gac	atg	gca	agg	ggc	atg	gcc	ttc	cta	cac	aca		1086
84	Val	Lys	Phe	Ala	Leu	Asp	Met	Ala	Arg	Gly	Met	Ala	Phe	Leu	His	Thr		
85	295		300		305		310											
86	cta	gag	ccc	ctc	atc	cca	cga	cat	gca	ctc	aat	agc	cgt	agt	gta	atg		1134
87	Leu	Glu	Pro	Leu	Ile	Pro	Arg	His	Ala	Leu	Asn	Ser	Arg	Ser	Val	Met		
88	315		320		325													
89	att	gat	gag	gac	atg	act	gcc	cga	att	agc	atg	gtc	aat	ttc			1182	
90	Ile	Asp	Glu	Asp	Met	Thr	Ala	Arg	Ile	Ser	Met	Ala	Asp	Val	Lys	Phe		
91	330		335		340													
92	tct	tcc	caa	tgt	cct	ggt	cgc	atg	tat	gca	cct	gcc	tgg	gta	gcc	ccc		1230
93	Ser	Phe	Gln	Cys	Pro	Gly	Arg	Met	Tyr	Ala	Pro	Ala	Trp	Val	Ala	Pro		
94	345		350		355													
95	gaa	gct	ctg	cag	aag	aag	cct	gaa	gac	aca	aac	aga	cgc	tca	gca	gac		1278
96	Glu	Ala	Leu	Gln	Lys	Lys	Pro	Glu	Asp	Thr	Asn	Arg	Arg	Ser	Ala	Asp		
97	360		365		370													

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98	atg tgg agt ttt gca gtg ctt ctg tgg gaa ctg gtg aca cgg gag gta	1326
99	Met Trp Ser Phe Ala Val Leu Leu Trp Glu Leu Val Thr Arg Glu Val	
100	375 380 385 390	
101	ccc ttt gct gac ctc tcc aat atg gag att gga atg aag gtg gca ttg	1374
102	Pro Phe Ala Asp Leu Ser Asn Met Glu Ile Gly Met Lys Val Ala Leu	
103	395 400 405	
104	gaa ggc ctt cgg cct acc atc cca cca ggt att tcc cct cat gtg tgt	1422
105	Glu Gly Leu Arg Pro Thr Ile Pro Pro Gly Ile Ser Pro His Val Cys	
106	410 415 420	
107	aag ctc atg aag atc tgc atg aat gaa gac cct gca aag cga ccc aaa	1470
108	Lys Leu Met Lys Ile Cys Met Asn Glu Asp Pro Ala Lys Arg Pro Lys	
109	425 430 435	
110	ttt gac atg att gtg cct atc ctt gag aag atg cag gac aag	1512
111	Phe Asp Met Ile Val Pro Ile Leu Glu Lys Met Gln Asp Lys	
112	440 445 450	
113	taggactgga aggtccttgc ctgaactcca gaggtgtcg gacatgggtt gggaaatgca	1572
114	cctccccaaa gcagcaggcc tctgggtgcc tccccccctt ccagtcatgg tactacccca	1632
115	gcctggggtc catccccctt ccccatccct accactgtgc gcaagaggggg cgggctcaga	1692
116	gcttgtcac ttgccacatg gtgtctccca acatgggagg gatcagcccc gcctgtcaca	1752
117	ataaaagttt atataaaaaaa aaaaaaaaaa aaaaaaaaaa	1789
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121 <212>	TYPE: PRT	
122 <213>	ORGANISM: H. sapiens	
123 <400>	SEQUENCE: 2	
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127	20 25 30	
128	His Gly Phe Ser Pro Leu His Trp Ala Cys Arg Glu Gly Arg Ser Ala	
129	35 40 45	
130	Val Val Glu Met Leu Ile Met Arg Gly Ala Arg Ile Asn Val Met Asn	
131	50 55 60	
132	Arg Gly Asp Asp Thr Pro Leu His Leu Ala Ala Ser His Gly His Arg	
133	65 70 75 80	
134	Asp Ile Val Gln Lys Leu Leu Gln Tyr Lys Ala Asp Ile Asn Ala Val	
135	85 90 95	
136	Asn Glu His Gly Asn Val Pro Leu His Tyr Ala Cys Phe Trp Gly Gln	
137	100 105 110	
138	Asp Gln Val Ala Glu Asp Leu Val Ala Asn Gly Ala Leu Val Ser Ile	
139	115 120 125	
140	Cys Asn Lys Tyr Gly Glu Met Pro Val Asp Lys Ala Lys Ala Pro Leu	
141	130 135 140	
142	Arg Glu Leu Leu Arg Glu Arg Ala Glu Lys Met Gly Gln Asn Leu Asn	
143	145 150 155 160	
144	Arg Ile Pro Tyr Lys Asp Thr Phe Trp Lys Gly Thr Thr Arg Thr Arg	
145	165 170 175	
146	Pro Arg Asn Gly Thr Leu Asn Lys His Ser Gly Ile Asp Phe Lys Gln	
147	180 185 190	

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148 Leu Asn Phe Leu Thr Lys Leu Asn Glu Asn His Ser Gly Glu Leu Trp
149 195 200 205
150 Lys Gly Arg Trp Gln Gly Asn Asp Ile Val Val Lys Val Leu Lys Val
151 210 215 220
152 Arg Asp Trp Ser Thr Arg Lys Ser Arg Asp Phe Asn Glu Glu Cys Pro
153 225 230 235 240
154 Arg Leu Arg Ile Phe Ser His Pro Asn Val Leu Pro Val Leu Gly Ala
155 245 250 255
156 Cys Gln Ser Pro Pro Ala Pro His Pro Thr Leu Ile Thr His Trp Met
157 260 265 270
158 Pro Tyr Gly Ser Leu Tyr Asn Val Leu His Glu Gly Thr Asn Phe Val
159 275 280 285
160 Val Asp Gln Ser Gln Ala Val Lys Phe Ala Leu Asp Met Ala Arg Gly
161 290 295 300
162 Met Ala Phe Leu His Thr Leu Glu Pro Leu Ile Pro Arg His Ala Leu
163 305 310 315 320
164 Asn Ser Arg Ser Val Met Ile Asp Glu Asp Met Thr Ala Arg Ile Ser
165 325 330 335
166 Met Ala Asp Val Lys Phe Ser Phe Gln Cys Pro Gly Arg Met Tyr Ala
167 340 345 350
168 Pro Ala Trp Val Ala Pro Glu Ala Leu Gln Lys Lys Pro Glu Asp Thr
169 355 360 365
170 Asn Arg Arg Ser Ala Asp Met Trp Ser Phe Ala Val Leu Leu Trp Glu
171 370 375 380
172 Leu Val Thr Arg Glu Val Pro Phe Ala Asp Leu Ser Asn Met Glu Ile
173 385 390 395 400
174 Gly Met Lys Val Ala Leu Glu Gly Leu Arg Pro Thr Ile Pro Pro Gly
175 405 410 415
176 Ile Ser Pro His Val Cys Lys Leu Met Lys Ile Cys Met Asn Glu Asp
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179 435 440 445
180 Met Gln Asp Lys
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184 <211> LENGTH: 258
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194 20 25 30
195 Cys Ile Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser
196 35 40 45
197 Val Met Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val

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198               50               55               60  
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 200               65               70               75               80  
 201 Lys Gly Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu  
 202               85               90               95  
 203 Gly Gly Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met  
 204               100              105              110  
 205 Glu Tyr Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg  
 206               115              120              125  
 207 Asn Val Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly  
 208               130              135              140  
 209 Leu Thr Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val  
 210               145              150              155              160  
 211 Lys Trp Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys  
 212               165              170              175  
 213 Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe  
 214               180              185              190  
 215 Gly Arg Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg  
 216               195              200              205  
 217 Val Glu Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala  
 218               210              215              220  
 219 Val Tyr Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg  
 220               225              230              235              240  
 221 Pro Ser Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His  
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 223 Glu Leu  
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 226 <211> LENGTH: 256  
 227 <212> TYPE: PRT  
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 231 <222> LOCATION: (1)...(256)  
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 236       20               25               30  
 237 Ile Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln  
 238       35               40               45  
 239 Glu Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu  
 240       50               55               60  
 241 Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met  
 242       65               70               75               80  
 243 Thr Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Glu Gly Lys Phe  
 244       85               90               95  
 245 Leu Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly  
 246       100              105              110  
 247 Met Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala

VERIFICATION SUMMARY  
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Input Set : N:\Crf3\RULE60\09840704.raw  
Output Set: N:\CRF3\12192001\I840704.raw

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L:188 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:230 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:271 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:314 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:357 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:367 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12